

FIG.1

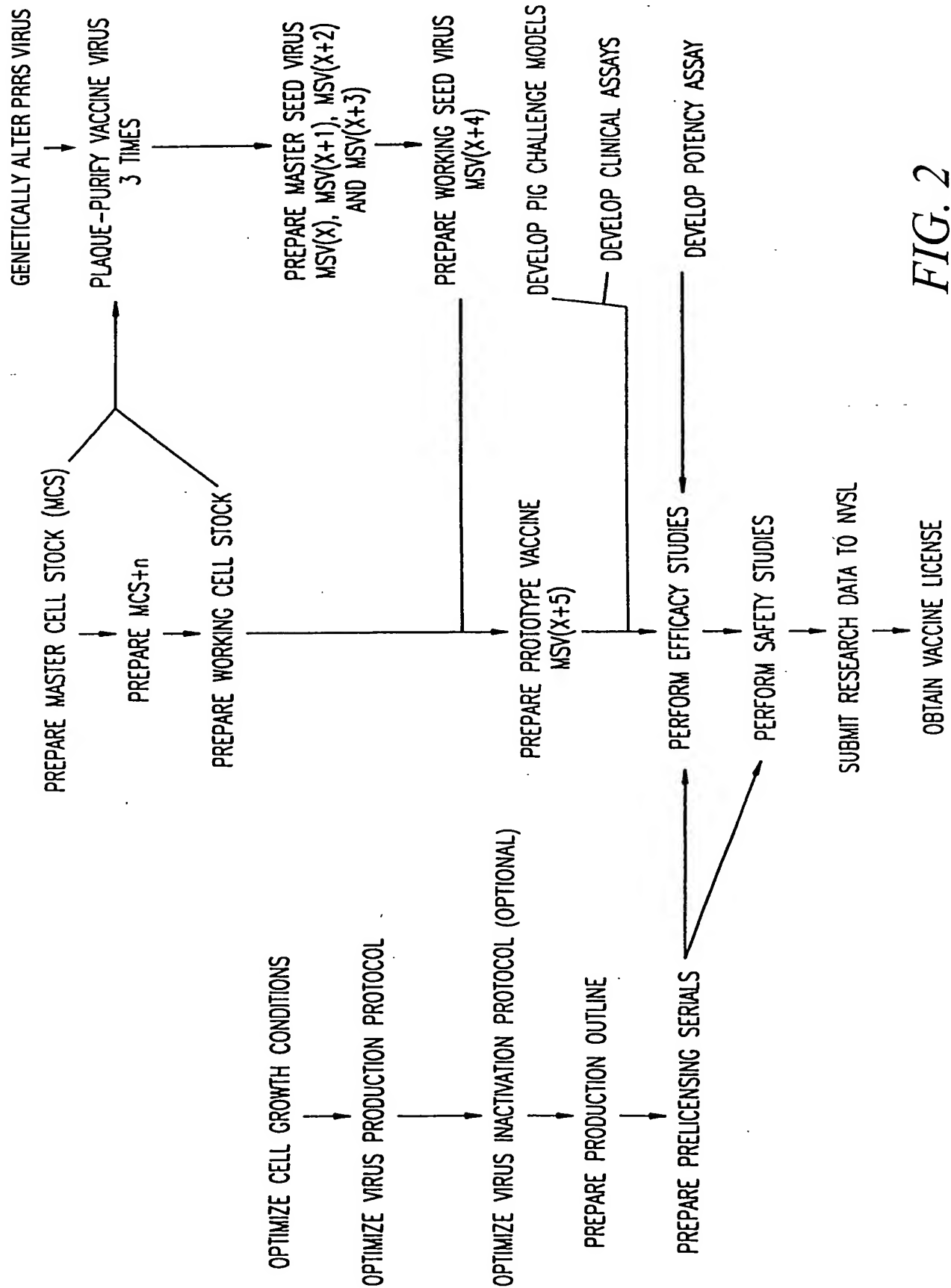


FIG. 2

FIG. 3A

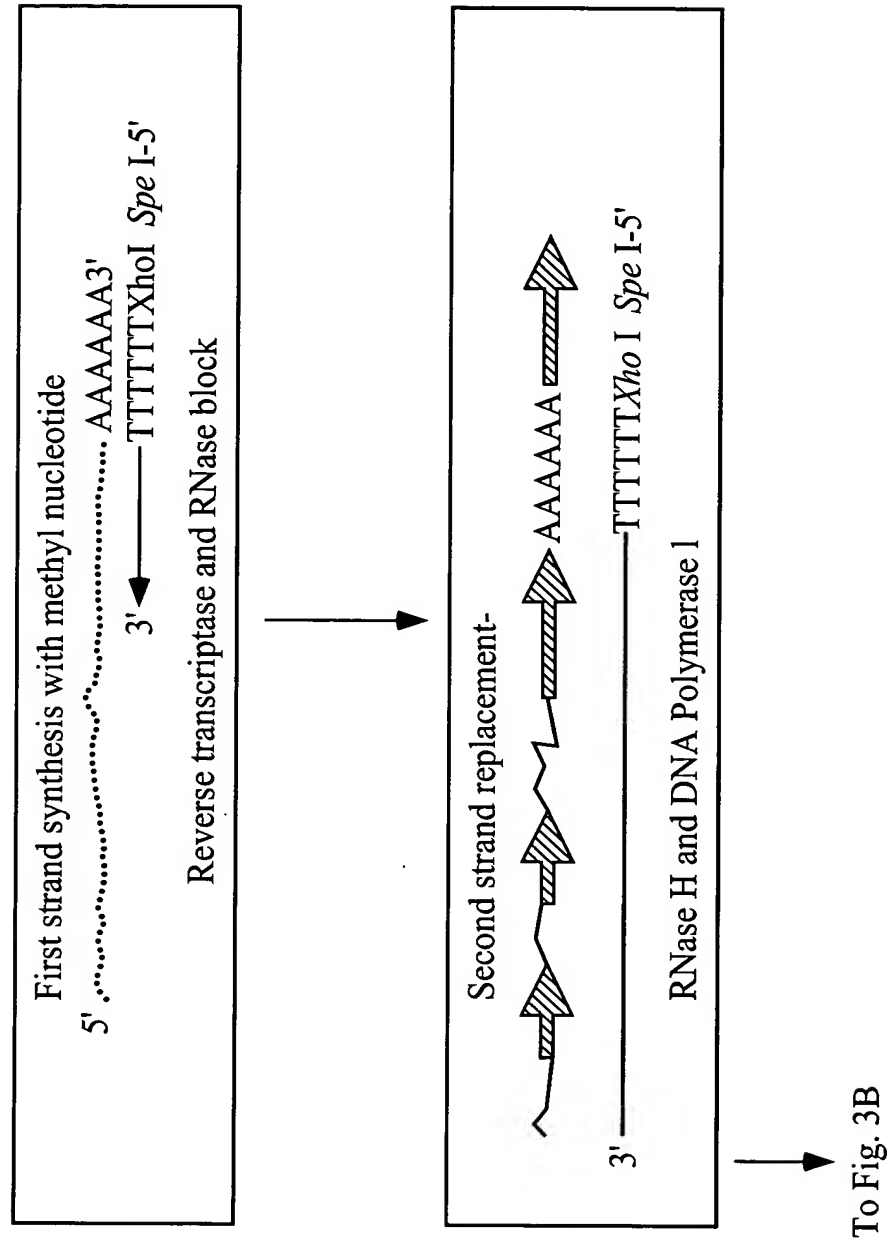
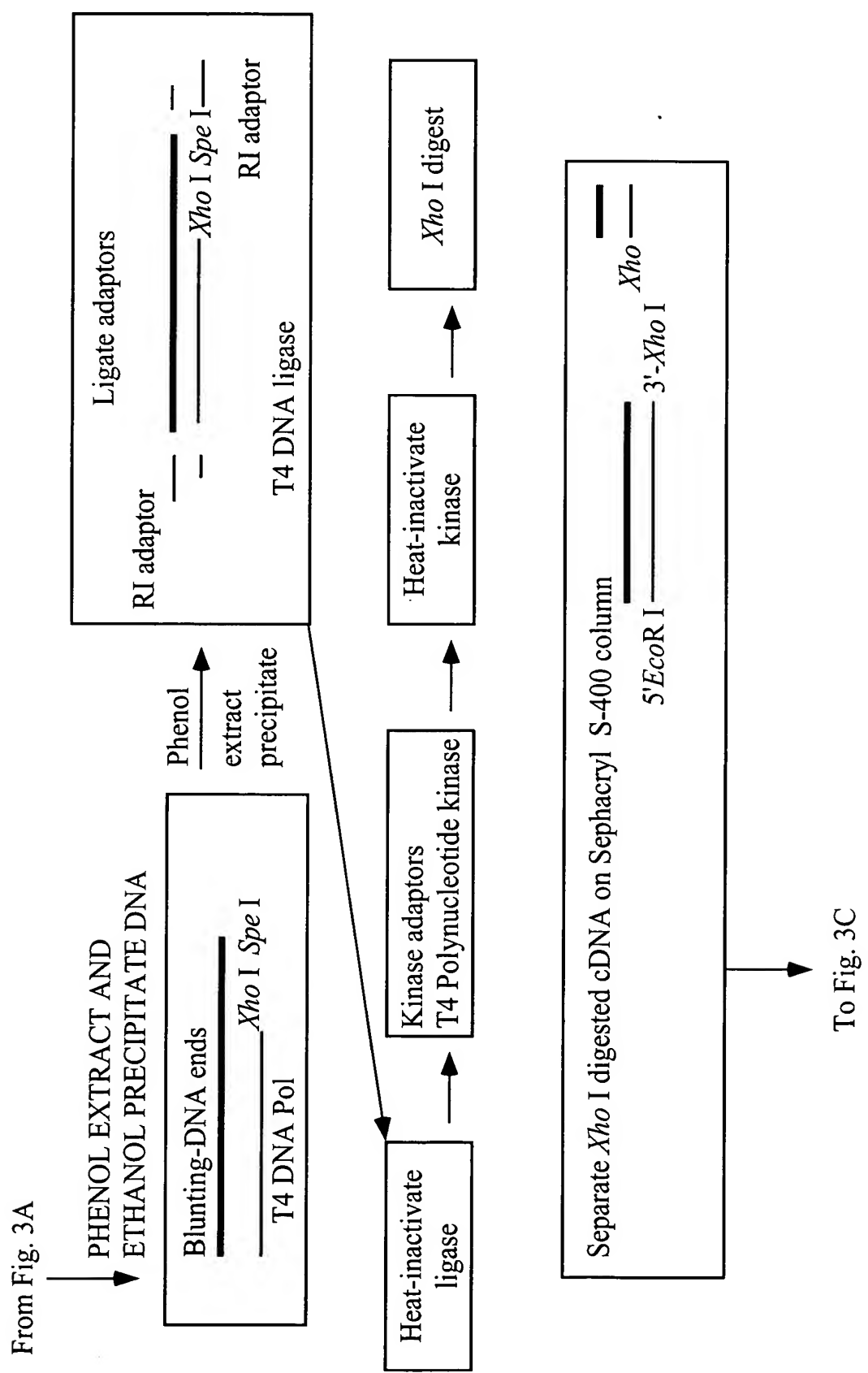


FIG. 3B



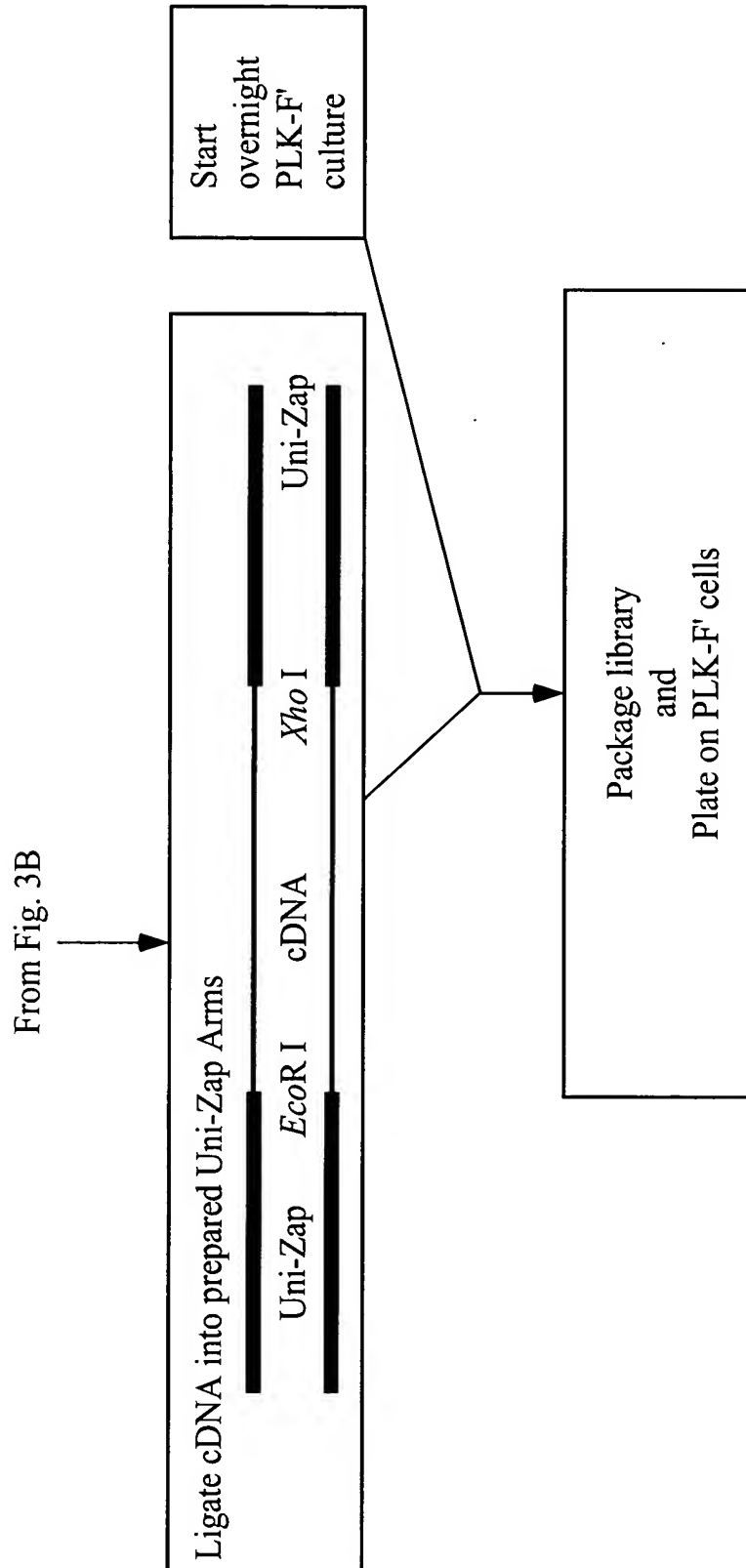


FIG. 3C

Identification of ISU-12 Authentic Clones by Differential Hybridization

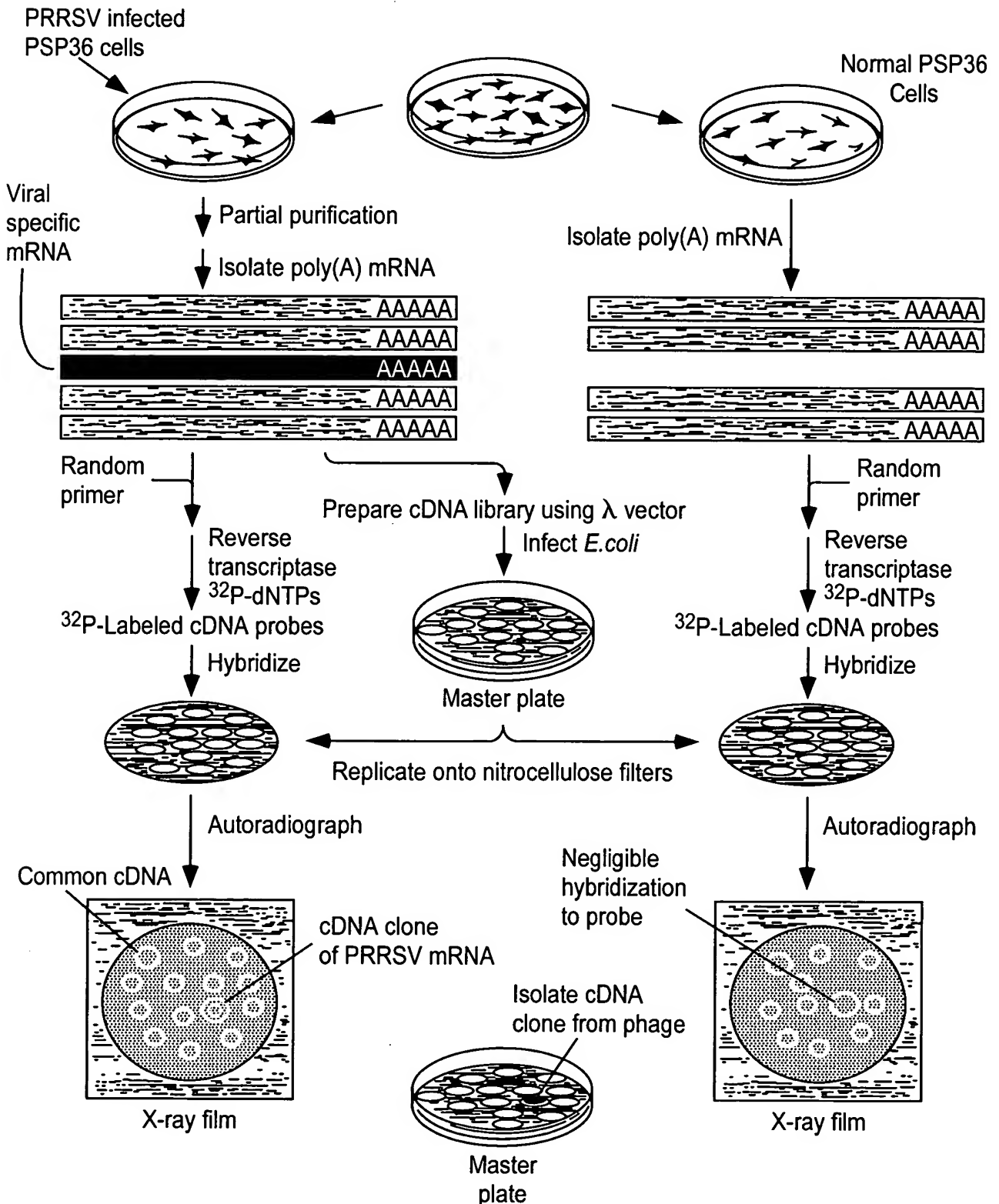


FIG. 4

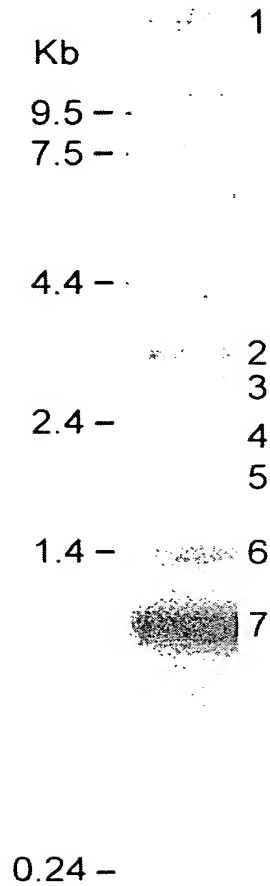


FIG. 5

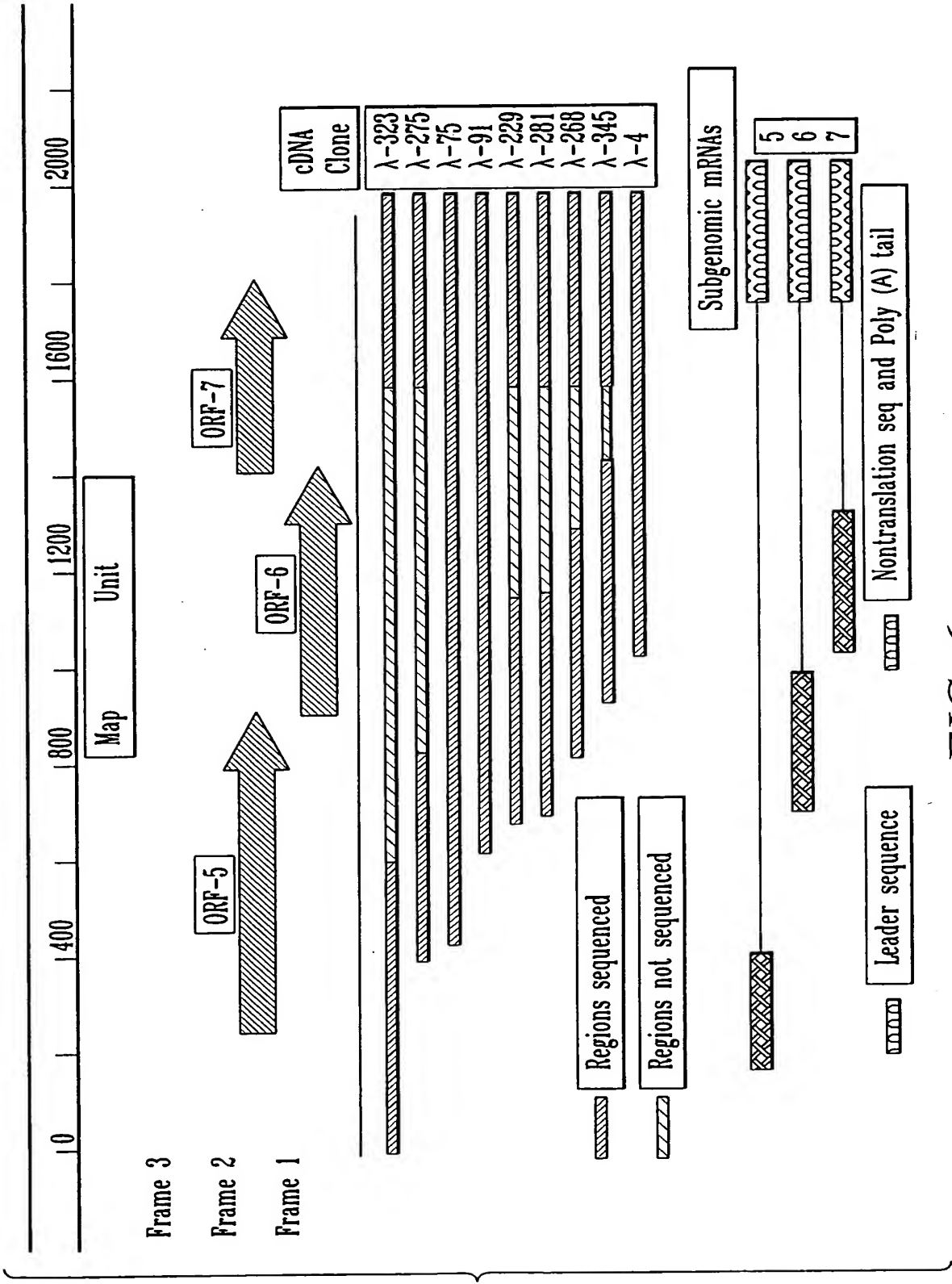


FIG. 6

GGCAGGCTTGGCTGCTCCAAAGACATCAGTTGCCCTTAGGCATGCGCAACTCGGCCCTCAGAGCGATTGCGAAAGTCCTCAGTGGCGGACGGCGGATAGGG 100
ACACCCGTGTATACACTGTCACAGCCAAATGTTACCGATGAGAAATATTGGCATCCCTCAGATCTTCATGCTTCTTCTTGGCTTTTCTATGCTTCTG 200
AGATGAGTGAAAGGATTTAAGGTGGTATTGGCAATGTGTACAGGCATCGTGGCAGTGTGGCTCAACTTACCAGTTACGTCCAACATGTCAGGAAATT 300
TACCCACGTTCCCTGGTAGTTGACCATGTGGGGCTGCTCCATTTTCATGACGCCGAGACCATGAGGTGGGCAACTGTTTTAGCCCTGCTTTTTTGGCATT 400
CTGTTGGCAATTGAAATGTTAAGTATGTTGGGAAATGCTTGACCGGGGCTGTTGCTCGCAATTGCTTTTTTGTGGTATCGTGGCGCTTGTGTTTT 500
GTTGGCGCTCGTCAGCGCCCAACGGGACAGCGGCTCAAAATTACAGCTGATTTACAACTTGACGCTATGTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600
AATTTGACTGGCAGTGGAGTGTTTTGTGATTTTTCCTGTGTTGACTCACATGTCTCTTATGGTGCCCTCACTACTAGCCATTCTTGGACACAGTCGG 700
TCTGGTCACGTGCTACCGCTGGGTTGTTACCGGGGGTATGTTCTGAGTAGCATGACGGGCTGTGCCCTGGCTGGCTTGAATTGCTTCGTCATT 800
AGGCTTGGGAAGAATTGCATGTCTGGCGCTACTCATGTACCAGATATACCAACTTCTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGGCTG 900
TCATCATAGAGAAAGGGGCAAAAGTTGAGGTGGAAGGTACCTGATCGACCTCAAAAGAGTTGTGTTGATGGTTCGGGGCTACCCCTGTAACCAGAGT 1000
TTCAGCGGAACAATGGAGTCGTCCTTAGATGACTTCGTGTCATGATAGCAGGCTCCACAAAGGTGCTCTTGGCGTTTCTATTACCTACACGCCAGTGA 1100

DRF4 stop

+1>DRF5 start

DRF6 start
+1> ***DRF5 stop

FIG. 7A

TGATATGCCC⁺TAAAGGTAGTCGCGCGCGACTGCTAGGGCTTC⁺TGCACCTTTTGGICTCCIGAATTGTGCTTTCACCTTCGGGTACATGACATTGCT 1200

GCAC⁺TT⁺CAGAGTACAAATAAGGTGCGGCTCACA⁺TATGGGAGCAGTAGTTGCAC⁺TCC⁺TTTGGGGGGTGTACTCAGCCATAGAAACCTGGAAATTCATCACC 1300

TCCAGATGCCGTTTGTGCTTGTAGCGCGCAAGTACATTCTGGCCCCCTGCCACCACGTTGAAAGTGC CGCAGGC⁺TTTCATCCGATTGGCGCAATGATA 1400

ACCACGCATTGTGCTCCGGGCTCCGGCTCCACTACGGTCAACGGCACATTGGTGC⁺CGGGTTAA⁺AAGCCTCGTGTGGGTGGCAGAAAAGCTGT⁺TAA 1500

DRF7 start
+1> ***DRF6 stop

ACAGGGAGTGGTAAACCTTGT⁺TAAATATGCCAAATAAC⁺CGGCAAGCAGAGAGAGAAAGAGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600

GCTGGGTAAAGTATCGCTACCCAAACCAAGTCCAGAGGCAAGGACCGGAAAGAAAAA⁺TAAAGAAAAACCCGGAGAGGCCCAATTTCCCTCTAGCG 1700

ACTGAAGATGATGTAGACATCAC⁺TTACCCCTAGTGAGCGTCAATTGTGCTGTCGTCATCCAGACCGCTTTAATCAAGGCGCTGGGACTTGCACCC 1800

***DRF7 stop

TGTCAGATT⁺CAGGGAGGATAAGTTACACTGTGGAGTTTAGTTTGCCTACGCATCATAC⁺TGTGGCCTGATCCGGCTCACAGCATCACCTCAGCATGATG 1900

GGCTGGCATTC⁺TGAGGCATCCAGTGT⁺TGAATTGGAAGAA⁺TGCGTGGTGAATGGCAC⁺TGATTGACATTGTGCCCTTAAGTCACCTATTCAATTAGGGC 2000

GACCGTGTGGGGTAAGATTTAATTGGCGAGAACCAACGCGCGAAATTAAAA⁺AAAAA 2062

FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACA	13556
ISU-12-3' TERMINAL (426-1028)	-----ATCTTGGGGAAATGCTT	485
	-----ATCTTGGGGAAATGCTT	
LELYSTAD SEQ (13484-14089)	---CCGCTTGTCTGCTT	13624
ISU-12-3' TERMINAL (426-1028)	GTGCCGCTTGTCTT	560
LELYSTAD SEQ (13484-14089)	ACCAATATGCGAGCTGAA	13699
ISU-12-3' TERMINAL (426-1028)	ACCAATATGCGAGCTGAA	635
LELYSTAD SEQ (13484-14089)	CCGCTTGGCACTCAAT	13774
ISU-12-3' TERMINAL (426-1028)	CCGCTTGGCACTCAAT	710
LELYSTAD SEQ (13484-14089)	GTATCCACTGCAAGAT	13849
ISU-12-3' TERMINAL (426-1028)	GTATCCACTGCAAGAT	785
LELYSTAD SEQ (13484-14089)	GTATGCTTGTGTCAT	13924
ISU-12-3' TERMINAL (426-1028)	GTATGCTTGTGTCAT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAG	13999
ISU-12-3' TERMINAL (426-1028)	GTGGACGACCGGGGAG	935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCACT	14073
ISU-12-3' TERMINAL (426-1028)	GGCAACCTCGTCACT	1009
LELYSTAD SEQ (13484-14089)	GGCAATGGGAGGCTTAG	14089
ISU-12-3' TERMINAL (426-1028)	GGCAATGGGAGGCTTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	AATCGAGTCG TCCATTACATG ACCTTGTCOA TGATAGCAGC GGTCCACAAA AGTTCCTCTT -ATGG-GACG --CGTAGACG ATTITITGCAA CGATCCCTATC GCGGCACAAA AGCTCGTGGT	947 14132
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	GGCGTTTCT ATTAACCTACA CCGCAGTCAT GATATATGCC CTAAAGGTGA GTCCGGGGCG ACCGTTTACC ATCAGATACA CACCTATTAAT GATATAGCC CTTAAAGGTGT CACGGGGCGG	1007 14192
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	ACTCTTAGGG CTCTCGCACC TTTTGGTCTT CTGAATTTGT GGTTTACCT TCGGTATACAT ACTCTCGGG CTGTTCGACA TCCTTAATATT TCTGAACGTGT TCGTTTACAT TCGGATACAT	1067 14252
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	GACATTCGTG CACTTTCAGA GTACAAATAA GTCCGGCTC ACTATGGGAG CAGTAGTTGC GACATATGTG CATTITCAAT CCACCAACCG TGTCCGACCTT ACCCTGGGGG CTGTTTGTGG-	1127 14311
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	ACTCTTTTGG GGGGTGTACT CAGC--CATTA GAACCTTGA AATTATCAC GTCCAGATGC -GGTTTCTGT GGGGTGTITA CAGCTTCACA GAGTCATGGA AGTTTATCAC TTCCAGATGC	1185 14370
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	CGTTTGTGCT TGTAGGCG CAAGTACATT CIGGGCCCTG CCAACCCAGT TCAAAGTGC AGATTGTCTT GCCTTGGCG GCGATACATT CIGGGCCCTG CCAATCAGT ACAAGTGT	1245 14430
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	GCAGGCTTTTC ATCCGATTC GGAATATGAT AACCAAGCAT TTTGTGTCG GCGTCCCGG GCAGGTCTCC ATTCAATCTC AGGTCTGCT AACCAAGCAT ACGCTCTGAG AAAGCCCGGA	1305 14490
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	TCCACTACG TCAACGGCAC ATTGGTCCC GGGTTAAAAA GCCTCGTGT GGTGCGCAGA CTACATCAG TCAACGGCAC TCTAGTACCA GGAATTCGGA GCCTCGTGT GGGGCGCAAA	1365 14550
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	AAAGCTGTTA AAGAGGAGT GGTAAACCTT GTTAAATATG CCAAAATAA CGAGCTGTTA AAGAGGAGT GGTAAACCTT GTTAAATATG GCGGTAA	1413 14598

FIG.9

Lelystad seq (14588 - 14974)	ATGCCCGGTA AAAACCAGCA- GCCCACAAGAA AAACAAGAAT A-CAG-----C	14632
ISU 12/7a/3' terminal (1403 - 1774)	-----AT GCGCAATTAAC ACCGGCAAGC AGCAGAAGAG	1434
Lelystad seq (14588 - 14974)	TCCCATTCGGG AATGCCCAGC CAGTCAATCA ACTGTCCCAAG TTGCTGGGTG	14681
ISU 12/7a/3' terminal (1403 - 1774)	AAACAATGGGG GATGCCCAGC CAGTCAATCA GCTGTCCCAAG ATGCTGGGTI-	1483
Lelystad seq (14588 - 14974)	CAATCATATAA GTCCCAAGCC CAGCAACCTTA GCGG--A-CG ACAGGCCAATA	14728
ISU 12/7a/3' terminal (1403 - 1774)	-AA-GATCAT CGGTCAACCAA AACCACTCA GAGGCAAGGG ACCGG---CA	1528
Lelystad seq (14588 - 14974)	AAGAAAAA-- ----A-----CCGAGCAAG CCACATTTTC CCTTGGGTGG	14766
ISU 12/7a/3' terminal (1403 - 1774)	AAGAAAAATA AGAAGAAAAA CCGCGAGCAAG CCGCATTTC GTCAGGAG	1578
Lelystad seq (14588 - 14974)	TGAAGATGAC ATCCCGCACC ACCTACCCCA CACTGACCCG TCCGTGTGCT	14816
ISU 12/7a/3' terminal (1403 - 1774)	TGAAGATGAT GTGAGACATC AGTTTACCCC TAGTGAGCGT CAATTGCTGC	1628
Lelystad seq (14588 - 14974)	TGCAATTCGAT CCAGACGGGT TTCAATCAAG GCGCAGGAAAG -TGGTTCCT	14865
ISU 12/7a/3' terminal (1403 - 1774)	TGTGCTCAAT CCAGACGGGC TTTAATCAAG GCGCTGGGAG TTGCAAG-CI	1677
Lelystad seq (14588 - 14974)	TTTCATCCAGC GCGAAGGTCA GTTTTACAGT TGAGTTATG CTGCCGGTTG	14915
ISU 12/7a/3' terminal (1403 - 1774)	GTCAGATTCA GGGAGGATTA GTTACACTGT GGAGTTAGT TTGCCGTACGC	1727
Lelystad seq (14588 - 14974)	CTCATAACAT CCGCCCTGATTT CCGGTACATTT CTACATCCGC CAGTCAGGT	14965
ISU 12/7a/3' terminal (1403 - 1774)	ATCATACTGT GCGCCCTGATC CCGGTACAG CATCACCG-T CAG-CATGA-	1774
Lelystad seq (14588 - 14974)	GCAGTTAA	14974
ISU 12/7a/3' terminal (1403 - 1774)		1774

FIG.10

ISU 12/7a/3' terminal (1775 - 1938)	TCGGCTGGCA TTCTTGAGGC ATCCAGTGT TTCAATTGGA	1814
Lelystad seq (14975 - 15101)	-----TT	14976
ISU 12/7a/3' terminal (1775 - 1938)	ACAAATGGTG GTGAATGGCA CTGATTGACA TTGTGCCCCTCT	1854
Lelystad seq (14975 - 15101)	TCACAGTCAG GTGAATGGCC GCGATTGGCG TGTGCCCCTCT	15016
ISU 12/7a/3' terminal (1775 - 1938)	AAGTCACCCTA TTCAATTAGG GCGAAGCTGT GGGGCTAACA	1800
Lelystad seq (14975 - 15101)	GAGTCACCCTA TTCAATTAGG GCGATCACAT GGGGCTCAATA	15056
ISU 12/7a/3' terminal (1775 - 1938)	TTTAATTGG CGAGAACCAC ACAGCCGAAA TTAAAAAAA	1933
Lelystad seq (14975 - 15101)	CTTAATCAGG CAGGAACCAT GTACCGAAA TTAAAAAAA	15096
ISU 12/7a/3' terminal (1775 - 1938)	AAAAA	1938
Lelystad seq (14975 - 15101)	AAAAA	15101

FIG. 11

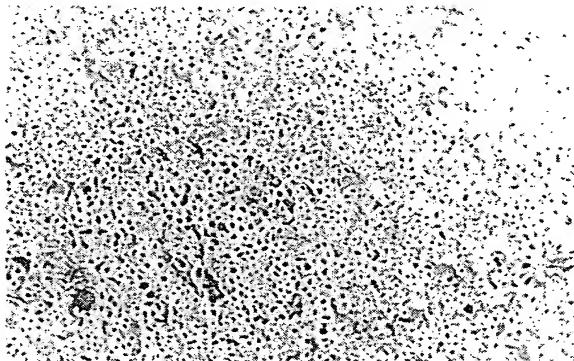


FIG. 12

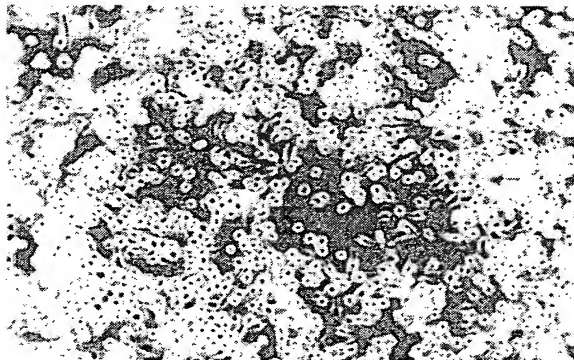


FIG. 13

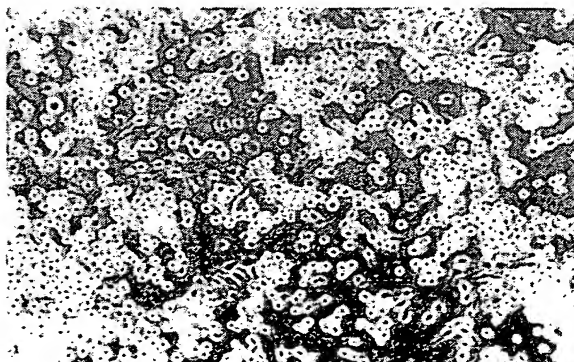


FIG. 14

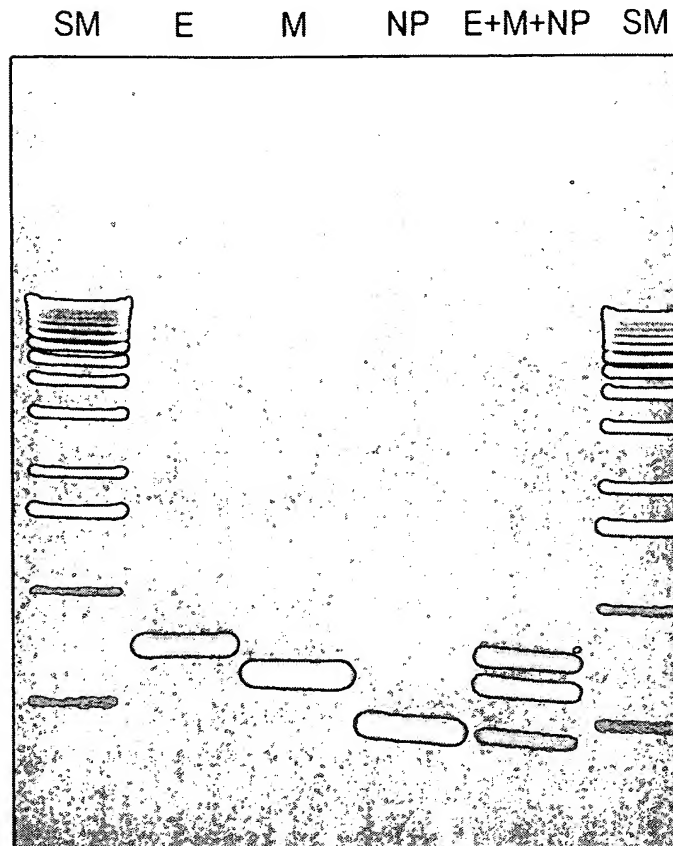


FIG. 15

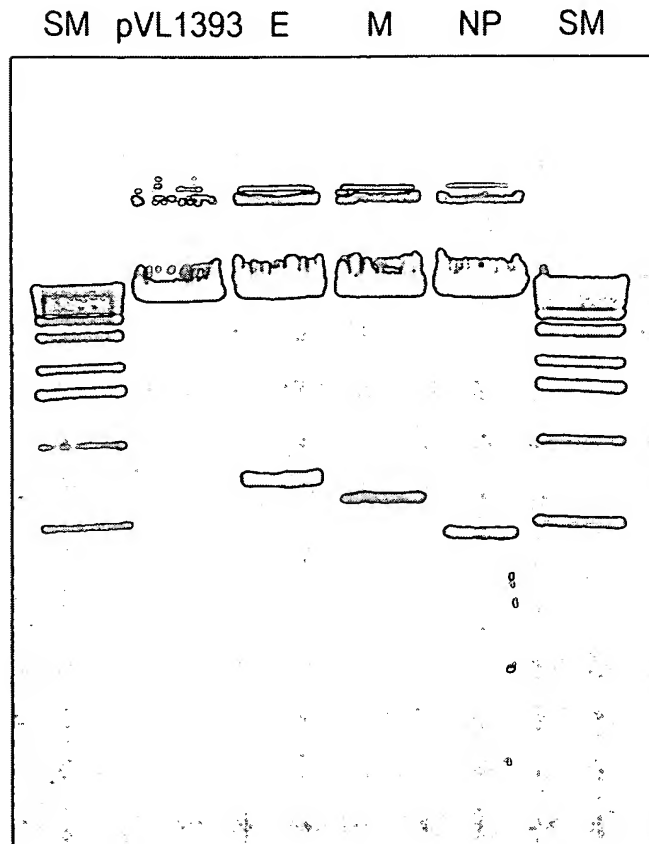


FIG. 16

DRF 6 start
+ 1>
VR 2385 AIGGAGTCGCTTAGATGACTTCCTGTCATGATAGCAGCGCTCCACAAAGGTGCTCTGGCGTTTCTATTACCTACACGCCAGTGATGATATATGCC 100
ISU-1894C.....T..... 100
ISU-22C.....T..... 100
ISU-79T.....T.....A..... 100
ISU-55C.....T.....C..... 100
ISU-3927C.....T.....G.....T..... 100
LVG--A..-G..C.....C..T..TC..CG.....C..CG..GC..A..C..AGC..C..A.....A..TA..A.....C..... 97
VR 2385 TAAAGTGAGTCGGCGGCGACTGCTAGGGCTTCGACCTTTTGGTCTTCCTGAATTGGCTTTCACCTTCGGGTACATGACATTCTGTCACCTTTCAGAG 200
ISU-1894A..... 200
ISU-22G.....A..... 200
ISU-79A..T.....C.....A..... 200
ISU-55A..A.....A.....A.....G..... 200
ISU-3927A.....A..T.....T.....T..... 200
LVTCA.....C..G.....GT.....A..CC..AA..A..T.....C..T..C..T..A.....A.....AT.....T.....ATC 197
VR 2385 TACAAATAAGTCGGCTCACTATGGGAGCAGTAGTTGCACCTCCTTTGGGGGGGTGTACTCAGC--CATAGAAACCTGGAAATTCATCACCCTCCAGATGCC 298
ISU-1894 298
ISU-22A..... 298
ISU-79 298
ISU-55C..... 298
ISU-3927C.....C.....T.....C.....TTA.....TT..C..GT..A.....G..T.....T.....A 295
LVC..C..CCGT.....A..T..CC.....G..T..T..C..--..CCT..C..T.....TTA.....TT..C..GT..A.....G..T.....T.....A 295

FIG. 17A

VR 2385	GT	T	G	T	G	T	G	C	C	G	C	A	G	T	T	C	G	C	C	T	T	C	G	G	A	A	T	G	A	T	A	A	C	C	G	C	A	T	T	398
ISU-1894	398	
ISU-22	398	
ISU-79	398	
ISU-55	398	
ISU-3927	395	
LV	A	
VR 2385	T	G	T	C	C	G	G	C	T	C	C	A	T	T	G	T	G	C	C	G	G	T	T	A	A	A	A	G	C	T	C	T	T	G	G	T	G	G	T	498
ISU-1894	498
ISU-22	498
ISU-79	498
ISU-55	498
ISU-3927	495
LV	C	
DRF 7 start																																								
VR 2385	G	T	A	A	C	T	T	G	T	T	A	A	T	A	T	G	C	C	A	A	T	A	C	C	G	G	C	A	-	A	G	C	A	G	A	G	A	A	582	
ISU-1894	582
ISU-22	582
ISU-79	582
ISU-55	582
ISU-3927	582
LV	591

FIG. 17B

VR 2385	CCAGATGCTGGGT--AA-GATCATCGCTCACCAAAACCAGTCCAGAGGCAAGGGACCGGGAAAGAAAAAATAAGAAAGAAAAACCCGGAGAGCCCCATTTC	679
ISU-1894--..-.....G.....C.....	679
ISU-22C--..-.....G.....T.....	679
ISU-79--..-.....C..G.....T.....	679
ISU-55--..-.....G.....C.....C.....	679
ISU-3927	...A.....--..-.....C..G.....T.....	679
LVT.....GC..T...A.AGT.C..G.---G....--..-CCT.G....---GCC.A.....G..T.....A.....	679

FIG. 17C

VR 2385	CTTGACC-CTGTCAGATTTCAGGAGGATAAGTTACACTGTGGAGTTAGTTTGCCTACGCATCATACTGTGGCCTGATCCGGGTCACAGCATCACCC-	877
ISU-1894T.....A.....T.....	877
ISU-22T.....	877
ISU-79T.....T.....	877
ISU-55T.....G.....G.....	877
ISU-3927C.....T.....T.....A.....G.....T.....G.....C.....	877
LVGT.....G.....T.....TCCAG.....A.....G.....T.....G.....TTTA.....T.....G	878

VR 23 85	TCAG-CA-----TGA	886
ISU-1894T.....	886
ISU-22T.....	886
ISU-79T.....	886
ISU-55T.....	886
ISU-3927T.....	886
LV	C.....T.....GGGTGCAAGT.A. ^^^^^^^^^^	898

*** DRF 7 stop

FIG. 17D

VR 2385 DRF6	MESSLDDFCHDSTAPQKVLLAFSITYTPVMYALKVSRGRLLGLLHLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAVVALLWGVSAIETWKFITSR	100
ISU-1894 DRF6	.G.....I.....	100
ISU-22 DRF6	.G.....I.....	100
SIU-55 DRF6	.G.....I.....	100
ISU-79 DRF6	.G.....Y.....M.....	100
ISU-3927 DRF6	.G.....N.....E..R.....	100
LV DRF6	.G-G.....N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S.....	99
PRRSV-10 DRF6	.G-G.....N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S.....	99
LDV-C DRF2	.G-G.-E..DQTSWY.-IFI...L...IA.S...F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL...I..V..I.TLVKIVDWLVI...	96
LDV-P DRF2	.G-G.-E..DQTSWY.-I.I...L...IA.S...F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..T...SL...I..V..I.TLVKIVNWMVL...	96
VR 2385 DRF6	LCLLGRKYILAPAHHVESAGGFHP1AANDNH-----AFVRRRPGSTTVNGTLVPGLKSLVLGGRKAVKQGVNVLVKY-AK	183
ISU-1894 DRF6-----	174
ISU-22 DRF6-----	174
SIU-55 DRF6-----	174
ISU-79 DRF6-----	174
ISU-3927 DRF6-----R.....K.....	174
LV DRF6	..C...R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR...R.....-GR	173
PRRSV-10 DRF6	..C...R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR...R.....-GR	173
LDV-C DRF2	..F...S.....PS.,D-----TSDGRQSLTTSITT.....K...L...Q...DFQR.....K...SK.A...L..VS.	171
LDV-P DRF2	..F...S.....PS.,D-----TSDGRQSLTTSITT.....K...L...Q...DFQR.....K...SK.A...L..VS.	171

FIG. 18A

VR 2385 DRF7 MPNNTGKQQRKK-----GDGQPVNQLCQMLGKIIAHQNSRGKGPCKKKNKKNPEKPHFPLATEDDDVRHHFTPSEQLCLSSIQTAFNQAGTCTLS 100
ISU-1894 DRF7N.....Q..... 93
ISU-22 DRF7N.....Q..... 93
ISU-79 DRF7N.....Q..... 93
ISU-3927 DRF7N...K.....Q.....I.. 93
ISU-55 DRF7N...K.....Q.....SG..... 93
VR2332 DRF7N...TEE.....Q..... 93
LV DRF7--A..N.SQ.,KKSTAPM,N.....L.,AM,KS,R,---QPR,GQA.,K.....A.,I.,L.QT.,S.,Q.....AS., 94
PRRSV-10 DRF7--A..N.SQ.,KKSTAPM,N.....L.,AM,KS,R,---QPR,GQA.,K.....A.,I.,L.QT.,S.,Q.....PS., 94
LDV-C DRF1SQ,KK,GGQN,-----AN,---N.LISALLRNAG,--N.,K.Q.K.,-Q.-L.,M.GPS,L.,VM.,N.V,M,R.,LV,L.,G.Q.,V 85
LDV-P DRF1SQ,KK,SGQN,-----AN,---N.LINALLRNAG,--N.,K.Q.K.,-Q.-L.,M.GPS,L.,VM.,N.V,M,R.,LV,L.,G.Q.,V 85
EAV DRF7ASRRSRP,AASF-----RN,R--RRQPTSVDLLRMFG,-----MRVR,PPAQPTQAI,EPG,L.,DLNQQ.,ATLS,NV,RF,MI,H,SL,-A 83
^^^^^^

VR 2385 DRF7 DSGRISYTFESLPHTHTVRLIRVTASP-----SA 134
ISU-1894 DRF7 123
ISU-22 DRF7 123
ISU-79 DRF7 123
ISU-3927 DRF7P,----- 123
ISU-55 DRF7 123
VR2332 DRF7 123
LV DRF7 S.,KV,FQ.,M.,VA.,.....STSASQAS 128
PRRSV-10 DRF7 S.,KV,FQ.,M.,VA.,.....STSASQAS 128
LDV-C DRF1G,NF.,S.M.,A.,...NAS,NS----- 115
LDV-P DRF1G,NF.,S.M.,A.,...NAS,NS----- 115
EAV DRF7A.GLT.,...SW-V.,KQIQ,KVAPP,G,----- 110
^^^^

FIG. 18B

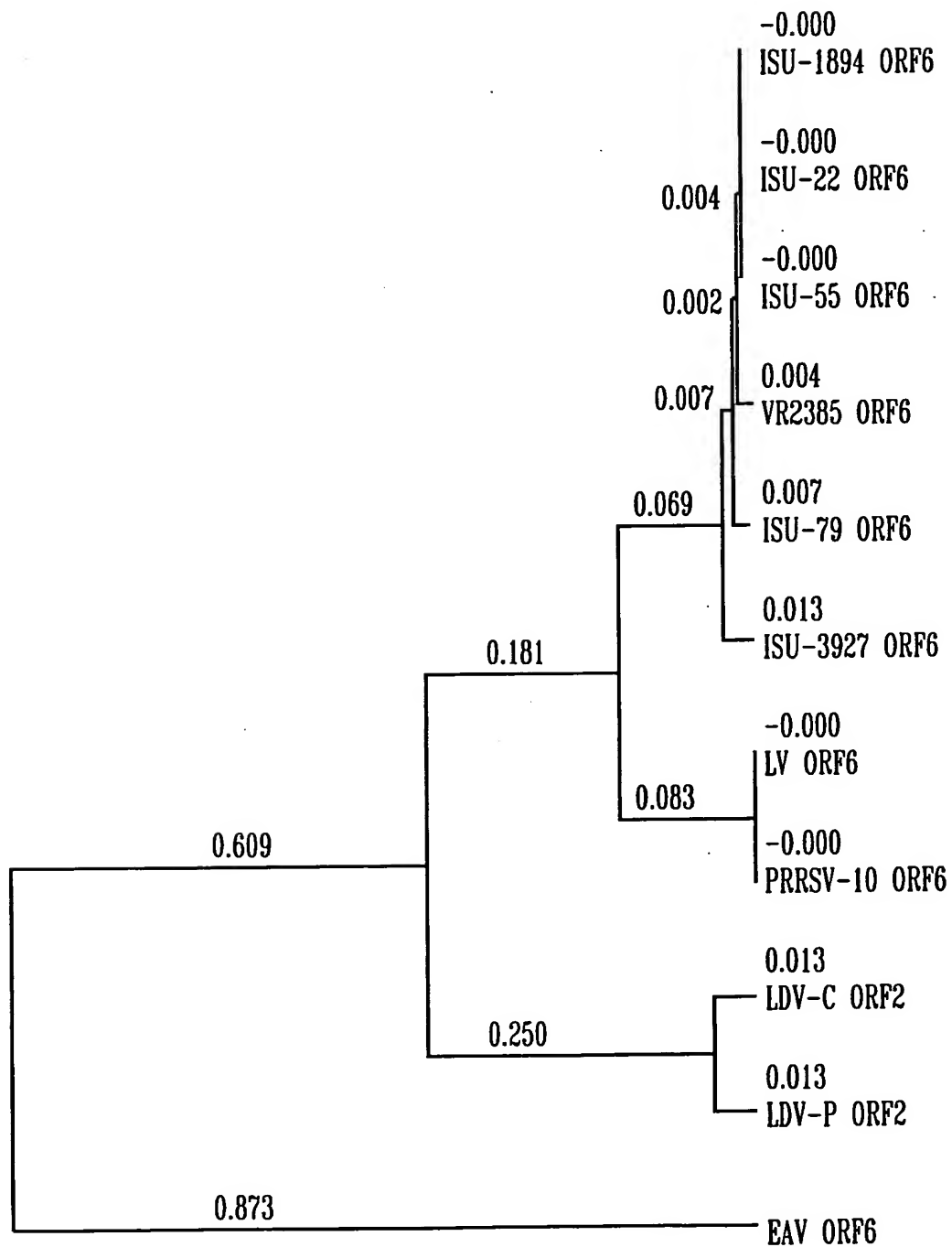


FIG. 19A

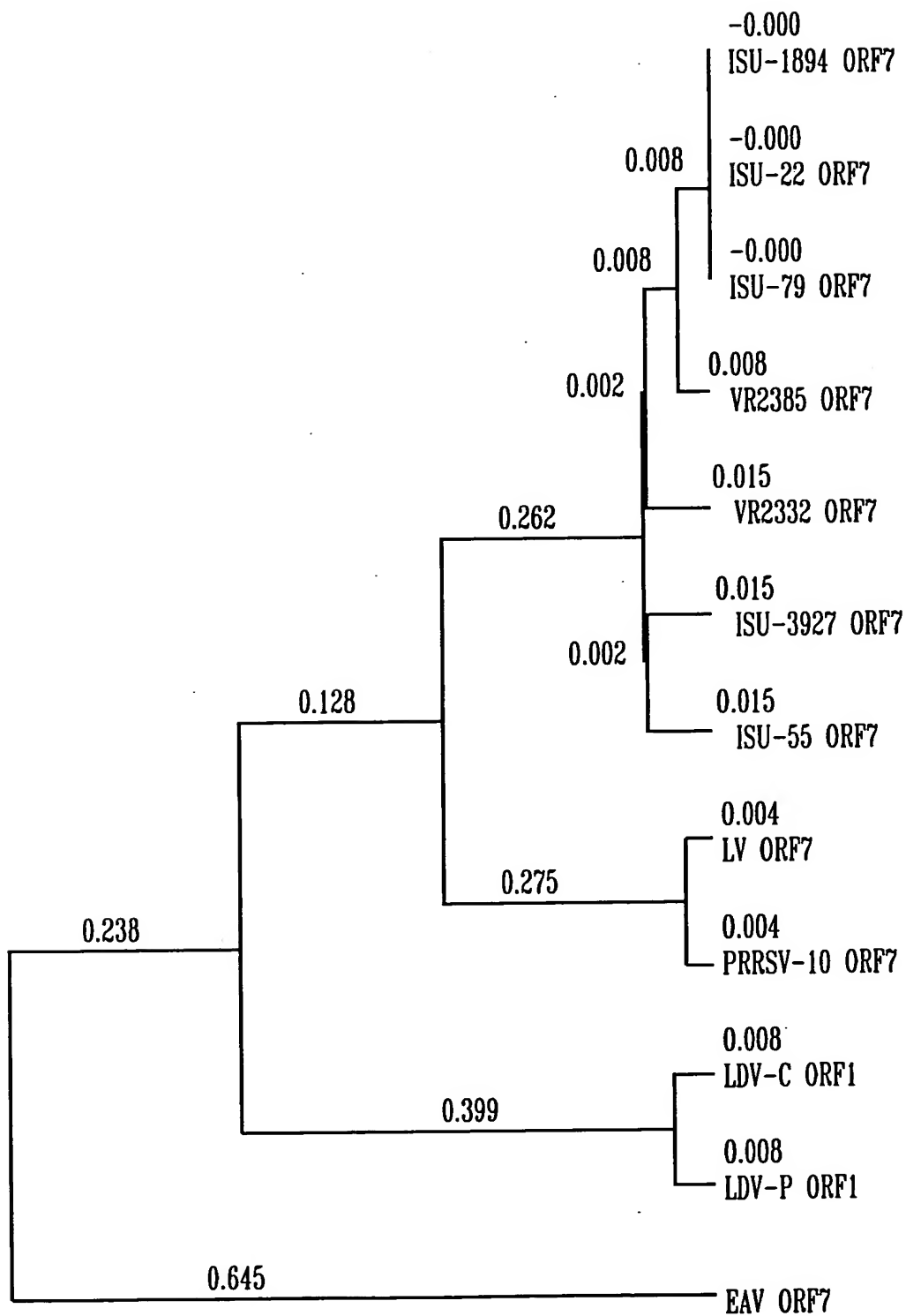


FIG. 19B

+ Start DRF2
100 CCTGAATTGAGATGAAATGGGGTCTATGCAAAAGCCTTTTGGACAAATGGCCAACCTTTTGTGGATGCTTTCACGGAGTCTTGGTGCCATTGTTGAT
200 ATCATTATATTTTGGCCATTTTGGCTTACCATCGCAGGTGGCTGGTCTTTTGCATCAGATTGGTTGGTCCGGGATACICCGTGGCGGCC
300 CTGCCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCTTTCTCTCAGTGCCAGGTGGACATTCCCACCTGGGGAACTAAACATCCTTTGGGGGA
400 TGCTTTGGCACCATAAGGTGTCAACCCTGATTGATGAAATGGTGTGGGTGCAATGTACCGCATCATGGAAAAAGCAGGACAGGCTGCCTGGAAACAGGT
500 AGTGAGCGAGGCTACGCTGTCTCGCATTAGTAGTTGGATGTGGTGGCTCATTTTCAGCATCTTGCCGCCATTGAAGCCGAGACCTGTAAATATCTGGCC
600 TCTCGGCTGCCCATGCTACACCACCTGGCGATGACAGGGTCAAAATGAACCATAGTGATATAAGTACTTTGAATCAGGTGTTTGCTGTTTTCCCAACCC
+ Start DRF3
700 CTGTTCCCGGCAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCCTCTATATTTTCTCTGTTCAGCTTCTTGACTCTTTTGTGTGT
800 GCTGTGTTGCGGGTTCCAATGCTACGTACTGTTTGGTTCCGCTGGTTAGGGCAATTTTCTTCGAACTCACGGTGAATTACACGGTGTGCCGC
*** Stop DRF2
900 CTTGCCTCACCCGGCAAGCAGCCGAGAGGCCACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGCGCATGATCGATGTGGGAGGACGATCATGATGA
1000 ACTAGGGTTGTGGTGGCGTCTGCCCTCCTCAGCGAAGGCCACTTGACCAGTGCTTACGGCTGGTTGGCGTCCCTGTCTTCAGCTATAGGCCAGTTC
1100 CATCCCGAGATATTCGGGATAGGGAAATGTGAGTCGAGTCTATGTTGACATCAAGCACCATTCAATTTGGGCTGTTTCATGATGGGAGAACACCACCTTGC

FIG. 20A

+ Start DRF4
CCCACCATGACAACATTTCAGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGAATTGGTTTCACCTAGATGGGTGGTCCCTTCTTTTC 1200
CTCTTGGTTGGTTTTAAATGTCCTCTTGGTTTCTCAGGCGTTCGCCTGCAAGCCATGTTTCAGTTCGAGTCTTTTCAGACATCAAGACCAACACCACCGCAG 1300
*** Stop DRF3
CGGCAGGCTTTGCTGCTCCTCCAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCTGAGGCGATTGCAAAAGTCCCTCAGTGGCGCAGGGGATAGG 1400
GACACCGGTATATCACTGTCACAGCCAATGTTACCGATGAGAAATTATTGCAATCCCTCTGATCTTCTCATGCTTTTCTTGGCTTTTCTATGCTTCT 1500
GAGATGAGTGAAAGGGATTTAAGGTGGTATTTGGCAATGTCAGGCATCGTGGCAGTGTGCGTCAACTTCACCAGTTACGTCCAACATGTCAGGAAT 1600
TTACCCACGTTCCCTTGGTAGTTGACCATGTGCGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCACTGTTTAGCCTGCTTTTACCAT 1700
*** Stop DRF4 + Start DRF5
TCTGTTGGCAATTGAAATGTTAAGTATGTTGGGGAAATGCTTGACCGGGGCTGTGCTCGCAATGCTTTTTTAAGGTGATCGTGCCGCTTGT 1799

FIG. 20B

Consensus	ATGMAATGGGGTCWMTGYRRAGCCTTTTGTGAYAAAATYRGCCARCTKTTYGTGGAYGCTTCACKGAGTTCYTKGKWSYRTKGTGTGATATYRYATWTT	100
VR2385 DRF2	...A...TA...CAA...C...TG...A...T...T...T...G...T...G...GTCCA...T...CATT...A...	100
LV DRF2	...C...AC...TGG...-----T...CA...G...G...C...C...T...T...TAGTG...G...TGGC...T...	91
Consensus	YYTKGCCATWYGTGTGGSTTCACCRICGAGGWTGGYTRSTGGTCTTTYKMYMCAGAKTGGTTTGCTCCGGMTWCTCCGTCGGGCYCTGCCATTAC	200
VR2385 DRF2	TT...G...TT...C...A...A...T...C...GG...TGCA...T...T...A...A...G...C...C...	200
LV DRF2	CC...T...AC...G...G...A...T...AC...CTTC...G...C...T...T...T...T...	191
Consensus	TCTSMSSAAYTAYMGAGRTCTATGARGSCCTTKYTSYCYMASTGCMRRSYGGAYAKTCCACAMTKKGSARYAARCAAYCCWTTGGGKATGYTTGGCA	300
VR2385 DRF2	...GAGC...T...CA...A...G...C...TC...CT...TC...G...CAGGT...C...T...-C...GG...G...ACT...A...T...T...G...C...	299
LV DRF2	...CCCG...C...TC...G...A...G...GT...GC...CA...C...AGACC...T-G...A...TT...C...GTC...G...C...A...T...T...	290
Consensus	CCATRMGAGTKTCMMMCYTGATTGATGARATGGTSTCKCGTCGMATKTACCRSAYCATGGAAWAKCAGGWCARGCKGCCTGGAAARCAGGTRGTRGYGA	400
VR2385 DRF2	...AA...-...G...AAC...C...A...G...G...A...G...A...G...T...A...G...T...A...A...A...GA...C...	398
LV DRF2	...-...GC...T...CCA...T...G...C...T...C...T...AG...C...T...T...T...A...G...G...G...G...TG...T...	389
Consensus	GGCYACGCTSTCWCGMAKYWGTCAGGKYTSGATRTGTRGTRKRCATTTTCARCAYCTKCCGCMRTKGARGCSGAKWCTGYMRMTWTCTSRSCTCWGCRC	500
VR2385 DRF2	...T...G...T...C...TTA...-...TT...G...G...G...G...T...T...T...T...CA...T...A...C...GA...C...TAAA...A...GGC...T...G...	496
LV DRF2	...C...-...C...A...A...GCT...GC...C...A...A...TA...C...A...C...G...AG...G...G...TT...T...CCGC...T...CAG...A...A...	487

FIG. 21A

Consensus	TSSYSATGCTAMAMMAYCTGYGCAYGWAGGGTCAAAATGTRASCMTASWGTAYAAAYASYACKTTGRAYCRSGTGTKWGTCTRTYTTCCCMACSCCWGGTW	600
VR2385 DRF2	.GCCC.....C.CC.C...C...T.AC.....A.C.A..GT...T..T.GT..T...A.T.AG...TT...-G.T.....A..C..T...T	595
LV DRF2	.CGTG.....A.AA.T..-T..-C.TT--..-.....G.G.C..CA...C..C.CC..G...G.C.GC..-GA.....A.C.....C..G..A...A	580
Consensus	CSMGGCCMAAGYTKMMYGATTTCMRRCATGGCTMATMRSTGTRCAYKCYTCYATWTTTCCCTCTGKGCWKCTCKKTACYYTKTTRTWGTCIKTG	700
VR2385 DRF2	.CC...A...C.TCAT.....CAG.....A..AGC...A..TT.C..T..A.....T...AG.T...TG...TC.T..TG.T.....G..	695
LV DRF2	.GA....C...T.GACC.....AGA.....C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT.G..CA.A.....T..	680
Consensus	GYTKCGRRTTCCARYKCTACGYWMTGTTTTTGGTTCCRYTGGYMRSGGCAAYWYWCWTTTCGARCTSACGGTGA	776
VR2385 DRF2	.T.G..GG.....ATG.....TAC.....GC...TAGG.....TTTT..T.....A..C.....	771
LV DRF2	.C.T..AA.....GCT.....CTA.....AT...CCCAC.....CACA..A.....G..G..-----	750

FIG. 21A. 1

Consensus	ATGGCTMATMRSTGRCAYKCYTCYATWTTTCCCTCTGTGKGCWKCCTKKTACYYTKTYRTWGTGCTKGGYTKCGRRTTCCARYKCTACGYWMTGTT	100
LV DRF3C..CAG...G..CG..T..C..T.....G..TT..A...GT...CT..G..CA..A...T...C..T..AA.....GCT.....CTA....	100
VR2385 DRF3A..AGC...A..TT..C..T..A.....T..AG..T...TG...TC..T...TG...T...G...T..G...GG.....ATG.....TAC....	100
Consensus	TTTGGTTCCRYTGGYMRSGGCAAYWYWCWTTTCGARCTSAACRTSAAYTACACSRTRTGCMYGCCYTGYYACCMGKCAAGCGCTCGCMRAREGCT	200
LV DRF3AT...CCCAC.....CACA..A.....G..G..CA..C...CA..A...AT...C..TTCT...A..T.....G.....CA..A..G..	200
VR2385 DRF3GC...TTAGG.....TTT...T.....A..C...GG..G..T.....GG..G...CC...T..CCTC...C..G.....A...-...AG..G..C..	199
Consensus	ACGARCCCGGMYGKWMCMTKTGGTGCARRATAGGGCATGAYMGRGTGTRGGAGSRYGAYCATGATGARYTAGKKWWTGTCRSRTSCCGTCYGGSYWCKMCA	300
LV DRF3	-...G.....TC..TAA..A..G.....AA.....CA..G.....CA..G...A...CGT..C.....GT..-..TTAA...CA..C.....C..GTA..GA..	298
VR2385 DRF3A.....CA..GTC..C..T.....GG.....TC..A....G....GAC..T.....AC...GGTT...-GG..G.....T..CCT..TC..	298
Consensus	SRGAMKSMMACTTGACSRGTMATTAYGCTGGYTGCTTGGCTYYTGTCCTTYWSTAYRCGGCCARTTCCATCCSGAGWTRTTCGGGATAGGGAATGTGWS	400
LV DRF3	A..--CTCAA.....-GG..TA...T..T...C...T..TTT.....TTC...CG.....A.....G...T..G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C...T....G..CCC.....CAG...TA.....G.....C...A..A.....AG	398
Consensus	KCGMGTCTWYGTGACAWSMRRACCARTTCATTGTGCGYGWKCATGATGGRCASAAVWCMACCKTRYCYMMCSRWSACACATYTCMGCMKTRYWTSMG	500
LV DRF3	G..C....TC..G...AGCGA.....G.....T..C..AG.....T..C..AG.....A..C..TT..A...G..AT..TAC..GGAC.....C..C..AT..ATA..GC..	495
VR2385 DRF3	T..A....AT..T....TCAAG.....A.....C..T..TT.....G..G..CA..C...T..GC..CCA..CATG.....T..A..CG..GCT..CA..	498

FIG. 21B

Consensus	RCMTATTACCASCAYCARRTMGACGGGGCAATTGGTTYCAYYTRGAATGGSTGGCKCCMYTCTTTTCYTCYTGGTGKTYTMAAYRTMTCTGTTTC	600
LV DRF3	G. A. C. C. AA. A. C. TT. G. C. G. AC. T. C. C. GC. C. CA. A. A.	595
VR2385 DRF3	A. C. G. T. GG. C. T. CC. A. G. T. CT. C. T. T. A. TT. A. TG. C. T.	598
Consensus	TSAGGGCTTGGCTGYAAGCCMTGTTTCWSKWCGMRCTCTWTCAGAYATYRAGACCAACACACCGRGCKGCMGGYTTYRYKGTCTCYCARGACATCART	700
LV DRF3	. G. T. C. TCGA. CA. A. T. TG. G. G. T. C. T. CATG. T. G. A.	695
VR2385 DRF3	. C. C. A. AGTT. AG. T. C. CA. C. A. G. A. C. TGCT. C. A. G.	698
Consensus	TGYTYMGRMTCACGGSRWCTCRGACGCKCANGAGRMRAATTCCTTCGSAAGTCGYCYCARTGCGYCGAMGSCGWYRGTACTCCCCAGTACATCAGCA	800
LV DRF3	. TT. CC. A. C. GGT. A. G. A. AAA. G. T. C. A. T. T. A. C. TCG.	795
VR2385 DRF3	. CC. TA. G. A. . ---. CAA. . G. --. T. -T. . GCG. -----C. T. G. C. C- C. G. ATA. -----	765
Consensus	TAA	803
LV DRF3	...	798
VR2385 DRF3	---	765

FIG. 21B.1

	100	100	100
Consensus	ATGGSTGGKCCMYTC	TTTTTCYTCYTG	GGTKYTMAYRTMCWTGGTTCTSAGCGCTTCGCC
VR2385 DRF4G...T...CT.....C...T...T...TT.A...TG.C...T.....C.....C.....A.....AGTT...AG...T.....C.		
LV DRF4C....G..AC.....T...C...C....GC.C...CA.A...A.....G.....T.....C.....TCGA...CA...A.....T.		

Consensus	TYRAGACCAACAC	SACCGCGCKGCMGGY	TTYRYKGTCTCYC	ARGACATCATTTG	YYTYMGR	CMTCACG	SGRWCTCRGC	AGCKCAW	AGRM	ATTTCC	CTT	200
VR2385	CAC.....	A..G..A..C..	TGCT.....	C..A.....	G...CC..TA..G..A..	---CAA...G..--T..T...	GC	GC	-----		189
LV	TGG.....	G..T..C..T..CATG.....	T..G.....	A...TT..CC..A..C.....	GGT...A....G..A...	AAA	AAA	AAA		200

	Consensus	CGSAAAGTCGTCYCGYRMGCSRTMGKACWCCSWGTTAYATCACKRTMACRCGYAAYGTKACCGAYGARWMTAYTTGYAYWCKCKGAYCTK	300
VR2385 DRF4	..C.....-C.T.,G.,C.,CACG.,GA,A.,G.,A.,GT...T.....TG.C.,A.,C.,T.,T.....T.,GAAT.,T.,,C.,TTC.T.,T.,T.,T	288	
LV DRF 4	..G.....T.C.,A.,T.,TGAA..CG.C.,T.,T.,CA.,,C.....GA,A.,G.,T.,C.,G.....C.,ATCA.,C.,,T.,CAA.G.G.,C.,,G	300	

	400C
Consensus	CTSATGCTTCTCKTGCC
VR2385 DRF4	CTATGCTTCTCKTGCC
LV DRF4	CTATGCTTCTCKTGCC

Consensus
VR2385 DRF4
LV DRF4

Consensus	MMKKRCMATGAGGTGGGCGACWRYVWTWGCYTGTYKTTYRCCATTCTTGGCAATWTGA	561
VR2385 QRF4	CGAGA, C, A, . TGTT, A, C, . C, T, . TA, G, T, . .	537
LV QRF4	ATCTG, A, T, . AACCA, T, . T, . G, . CG, C, A, . .	552

FIG. 21C

Consensus	M, WG, C, K, L, W, L, SL, P, CL, SPSQ, G, WSF, S, WFAPR, SVRALPFTL, NYRRSYE, L, C, D, P, KH	100
LV DRF2,	. Q, . H, GV, SASCSWTPS, SSSLV, LI-----, PF, Y, G, D, Y, F, E, P, GL, PN, RP, V, QFAY, . .	90
VR2385 DRF2,	. K, . L, --, ----AFLTK, AN-FL, MLSSSWCP, LI, YFW, F, A, D, Y, S, AF, SQ, QV, I, TWGT, . .	93
Consensus	PLGM, WH, . VS, LIDEMVSRR, Y, . ME, . . GQAANKQVV, EATL, S, LD, V, HFQHLAA, EA, C, L, SRL, ML, NV, YN, TL, V,	200
LV DRF2, F, MR, . H, I, QT, . HS, G, TKL, G, . I, T, V, DS, RF, S, V, KN, AV--G, . SLQ, . T, . . DR, ELI	188
VR2385 DRF2, L, . HK, . T, M, RI, . KA, S, SRI, S, . V, A, I, . ET, KY, A, P, HH, RMTGS, . TIV, . S, . . NQ, FAV	193
Consensus	FPTPG, RPKL, DF, QWLI, VH, SIFSSVA, S, TLF, VLWLR, P, LR, VFGF, W, . A,	264
LV DRF2, T, T, . R, S, . A, S, V, I, I, A, . Y, H, PT, ---THSS	249
VR2385 DRF2, S, H, . Q, A, . S, A, C, V, V, M, . T, R, LG, IFLNSNR-	257

FIG. 22A

Consensus MA., C., ..., FLC., ..., Y., ..., A., ..., S., T., CFWFPL., GN. SFELT, NYT, C. PC, T. QAA., ..., EPGR., WC, IGHDRC, E, DHDEL., ..., PSG., ... 100
 LV DRF3, .. HQ, ARFHF., ..., GFIC, LVHS, LASN, SS, L., ..., AH., T., ..., I., I., M., S., S., RQRL., ..., NM., K., ..., E. R., ..., LMSI., ..., YDN 100
 VR2385 DRF3, .. NS, TFLYI., ..., CSFL, SFCC, VWAG, NA, Y., ..., VR., F., ..., V., V. P., L. R., AEAY., ..., SL., R., ..., G. D., ..., GFW., ..., LSS 100

Consensus ... L., YAWLA, LSFSY, AQFHPE, FGIGNVSRV, VD., HQFICA, HDG, N, T., ..., NISA., ..., YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL 200
 LV DRF3, L-K, EGY., ..., F., ..., A., ..., L., ..., F., KR., ..., E., H, S, VSTGH., ..., LYAA., H., I., ..., L., ..., I., ..., 199
 VR2385 DRF3, EGH, TSA., ..., S., ..., T., ..., I., ..., Y., IK., ..., V., Q, T, LPHHD., ..., VLQT., Q., V., ..., V., F., ..., V., ... 200

Consensus RRSP, S, VS, R., Q., RPT, P., ..., S., TS., ..., L., ..., R, F., ..., K, S., ... 266
 LV DRF3, V, P., R, IY, IL., ..., R, RLPVSW, FR., IVSD, TGSQQRK, K, PSESPPNVV, P, VLPSTR 265
 VR2385 DRF3, A, H., V, VF, TS., ..., P, QRQALL, SK., V--A, GIATRPL, R, A-----, -, LSAARR- 255

FIG. 22B

Consensus M, A., LF, L, G., ..., VS, AFACKPCFS., LSDI, TINTAAGF, VLQDI, C, R., ..., A, E, I., K., QCR, A, GTP, YIT, TANVTDE, YL., ..., DL 100
 LV DRF4, , A, AT., F, A, AQHIM., E., ..., TH., ..., E., ..., M., ..., N, F, PHGVA, Q, K, SFG, SS., E, V., Q., I., ..., S., YNA., ... 100
 VR2385 DRF4, , G, SL., L, V, FKCLL., Q., ..., SS., K., ..., A., ..., S, L, HR--NS, S, A, R--, VP., T, I., V., V., ..., N., HSS., ... 96

Consensus LMLS, CLFYASEMSEKGFV, FGNVSG, V., CVNFT, YV, HV., ..., TQ., ..., V., ..., RLLHF, TP., MRWAT., ACLF, ILLAI, 184
 LV DRF4, A., ..., I., ..., V, SA., ..., D., A., TQH., QHHL, IDHI., ..., L., SA., ..., TI., ..., A., ... 183
 VR2385 DRF4, S., ..., V., ..., I, AV., ..., S., Q., KEF., RSLV, DH-V., ..., M., ET., ..., VL., ..., T., ... 179

FIG. 22C

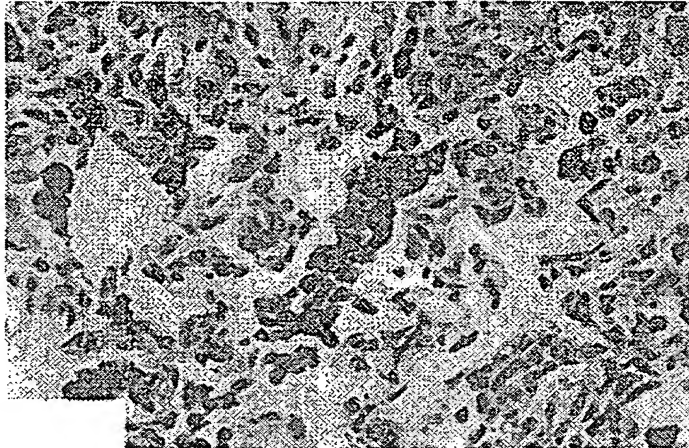


FIG. 23

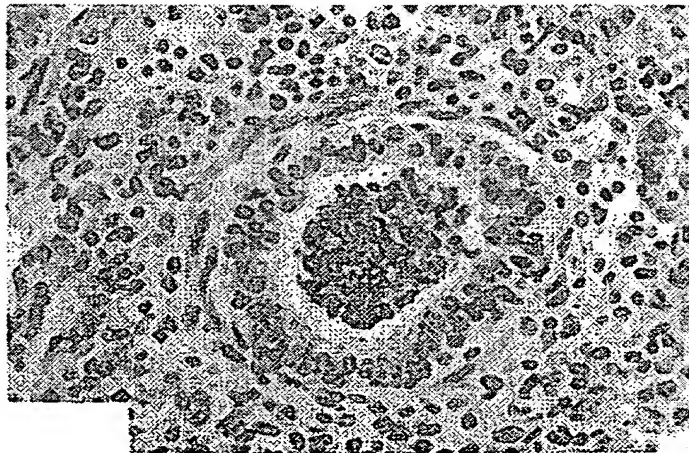


FIG. 24

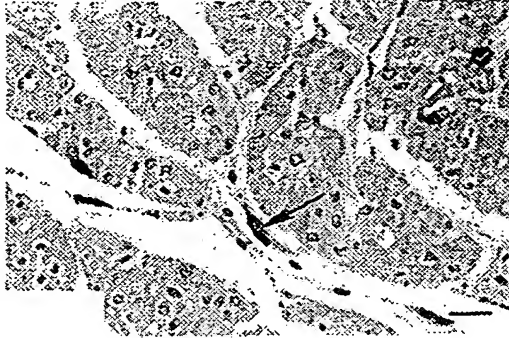


FIG. 25

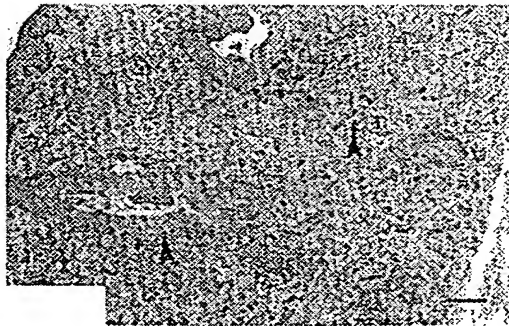


FIG. 26

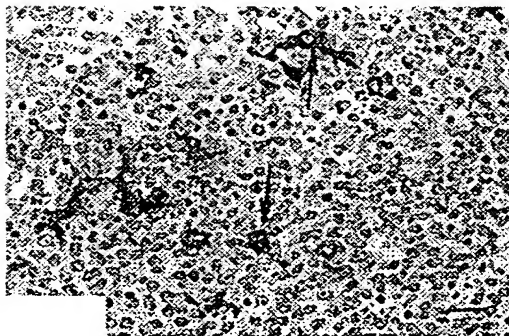


FIG. 27



FIG. 28A

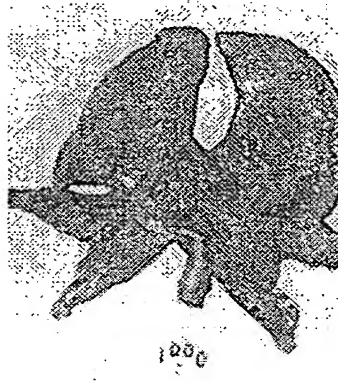


FIG. 28B

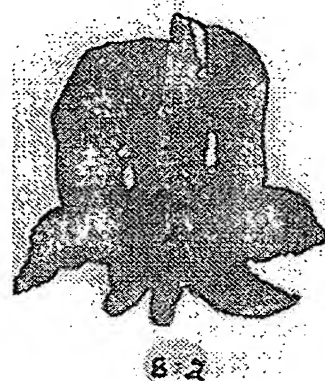


FIG. 28C

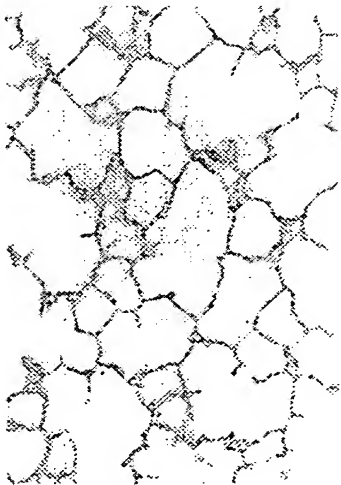


FIG. 29A

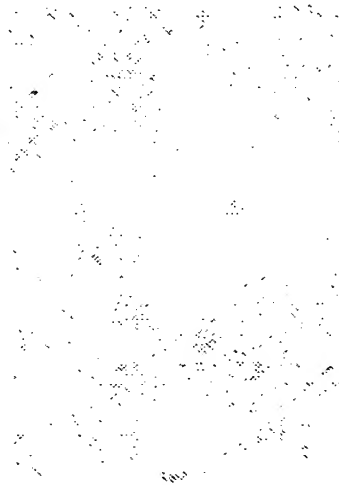


FIG. 29B

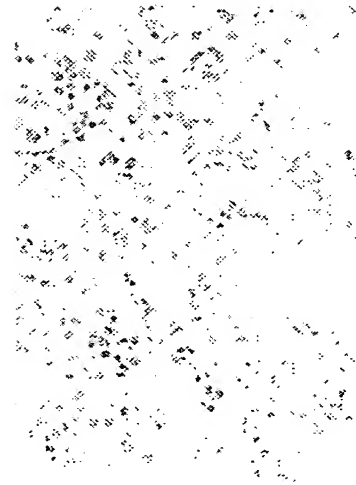


FIG. 29C

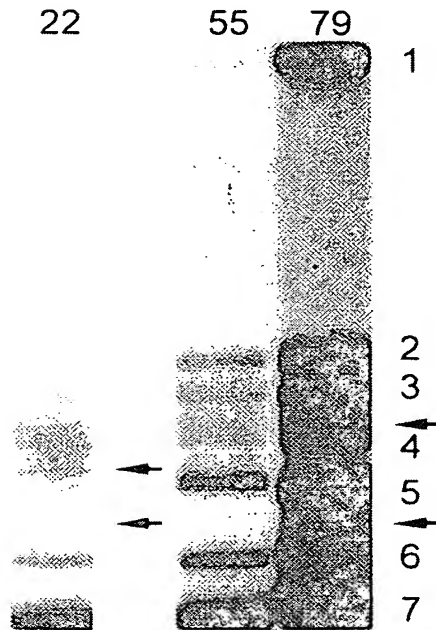


FIG. 30A

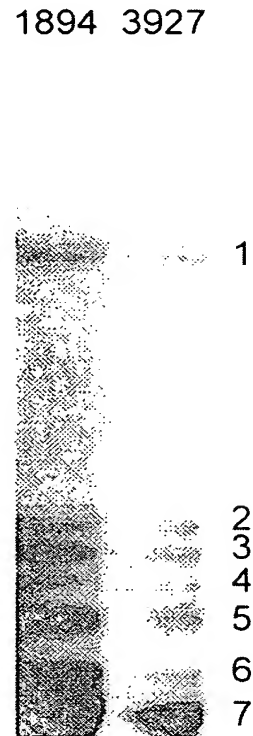


FIG. 30B